

FIG. 1

ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG TTT ACG GTC AGT TTG GCA	48
Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala	
1 5 10 15	
TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT CAA AGA GAG AAA CAT AAC	96
Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn	
20 25 30	
GGC GGT AGA GGG GAA GTC ACC AAG GTT GCC ACT CAG AAG CAC CGA CAG	144
Gly Gly Arg Gly Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln	
35 40 45	
TCA CCG CTT AAC TGG ACC TCC AGT CAT TTC GGA GAG GTG ACT GGG AGC	192
Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser	
50 55 60	
GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC CCC TAC TCC CGG GCT TTC	240
Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe	
65 70 75 80	
GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC TGC AGG AAC GGC GGT ACC	288
Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr	
85 90 95	
TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG GCC CAC TTC ACC GGC CGC	336
Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg	
100 105 110	
TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA TGC GGC GCC CTG GAG CAC	384
Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His	
115 120 125	
GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC TGC AGG TGC ATC TTC GGG	432
Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly	
130 135 140	
GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT GAC CGC TGT GAC CCG AAA	480
Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys	
145 150 155 160	
GAC TTC CTG GCC TCC CAC GCT CAC GGG CCG AGC GCC GGG GGC GCG CCC	528
Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro	
165 170 175	
AGC CTG CTA CTC TTG CTG CCC TGC GCA CTC CTG CAC CGC CTC CTG CGC	576
Ser Leu Leu Leu Leu Leu Pro Cys Ala Leu Leu His Arg Leu Leu Arg	
180 185 190	
CCG GAT GCG CCC GCG CAC CCT CGG TCC CTG GTC CCT TCC GTC CTC CAG	624
Pro Asp Ala Pro Ala His Pro Arg Ser Leu Val Pro Ser Val Leu Gln	
195 200 205	
CGG GAG CGG CGC CCC TGC GGA AGG CCG GGA CTT GGG CAT CGC CTT TAA	672
Arg Glu Arg Arg Pro Cys Gly Arg Pro Gly Leu Gly His Arg Leu *	
210 215 220	

FIG. 2

AMINO ACID ALIGNMENT BETWEEN CRIPTO AND CRIPTIN

		10		20		30		40																																		
1		M	T	W	R	H	H	V	R	L	L	F	T	V	S	L	A	L	Q	I	I	N	L	G	N	S	Y	Q	R	E	K	H	N	G	G	R	G	E	V	T	K	HGS Cryptin
1		M	-	-	H	A	A	I	S	K	V	F	E	L	G	L	-	-	-	V	A	G	L	G	-	-	-	H	Q	E	F	A	R	P	S	R	G	Y	L	A	-	Human Cripto
		50		60		70		80																																		
41		V	A	T	Q	K	H	R	Q	S	P	L	N	W	T	S	S	H	F	G	E	V	T	G	S	A	E	G	W	G	P	E	E	P	L	P	Y	S	R	A	F	HGS Cryptin
32		-	-	-	-	F	R	D	D	S	I	-	W	P	Q	E	E	-	P	A	I	R	P	R	S	S	Q	R	V	P	P	M	G	I	Q	H	S	K	E	L	Human Cripto	
		90		100		110		120																																		
81		G	E	G	A	S	A	R	P	R	C	C	R	N	G	G	T	C	V	L	G	S	F	C	V	C	P	A	H	F	T	G	R	Y	C	E	H	D	Q	R	R	HGS Cryptin
65		N	R	T	-	-	-	-	-	-	C	C	L	N	G	G	T	C	M	L	G	S	F	C	A	C	P	P	S	F	Y	G	R	N	C	E	H	D	V	R	K	Human Cripto
		130		140		150		160																																		
121		S	E	C	G	A	L	E	H	G	A	W	T	L	R	A	C	H	L	C	R	C	I	F	G	A	L	H	C	L	P	L	Q	T	P	D	R	C	D	P	-	HGS Cryptin
99		E	N	C	G	S	V	P	H	D	T	W	L	P	K	K	C	S	L	C	K	C	W	H	G	Q	L	R	C	F	P	Q	A	F	L	P	G	C	D	G	L	Human Cripto
		170		180		190		200																																		
160		-	-	-	K	D	F	L	A	S	H	A	H	G	-	P	S	A	G	G	A	P	S	L	I	L	L	L	P	C	A	L	L	H	R	L	L	R	P	D	A	HGS Cryptin
139		V	M	D	E	H	L	V	A	S	R	T	P	E	L	P	P	S	A	R	T	T	T	F	L	M	V	G	I	C	L	S	I	Q	S	Y	-	Human Cripto				
		210		220																																						
196		P	A	H	P	R	S	L	V	P	S	V	L	Q	R	E	R	R	P	C	G	R	P	G	L	G	H	R	L	-	-	-	-	-	-	-	-	-	-	-	-	HGS Cryptin
174		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Human Cripto	

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.